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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=6; day=24; hr=12; min=19; sec=54; ms=228;]

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Application No: 10593265 Version No: 2.0

Input Set:

Output Set:

Started: 2011-06-15 18:23:14.517
Finished: 2011-06-15 18:23:16.705
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 188 ms
Total Warnings: 24
Total Errors: 0
No. of SeqIDs Defined: 24
Actual SeqID Count: 24

Error code	Error Description
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Error code	Error Description
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SEQUENCE LISTING

<110> COMISSARIAT A L'ENERGIE ATOMIQUE
RICHAUD, Pierre
VERRET, Frederic
GRAVOT, Antoine
AUROY, Pascaline
VAVASSEUR, Alain

<120> GENETICALLY MODIFIED PLANTS AND THEIR APPLICATIONS IN
PHYTOREMEDIATION

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Met Ala Leu Gln Asn
1 5
114

aaa gaa gaa gag aaa aag aaa gtg aag aag ttg caa aag agt tac ttc 162
Lys Glu Glu Glu Lys Lys Val Lys Lys Leu Gln Lys Ser Tyr Phe
10 15 20

gat gtt ctc gga atc tgt tgt aca tcg gaa gtt cct ata atc gag aat 210
Asp Val Leu Gly Ile Cys Cys Thr Ser Glu Val Pro Ile Ile Glu Asn
25 30 35

att ctc aag tca ctt gac ggc gtt aaa gaa tat tcc gtc atc gtt ccc 258
Ile Leu Lys Ser Leu Asp Gly Val Lys Glu Tyr Ser Val Ile Val Pro
40 45 50

tcg aga acc gtg att gtt gtt cac gac agt ctc ctc atc tct ccc ttc 306
Ser Arg Thr Val Ile Val Val His Asp Ser Leu Leu Ile Ser Pro Phe
55 60 65

caa att gct aag gca cta aac gaa gct agg tta gaa gca aac gtg agg 354
Gln Ile Ala Lys Ala Leu Asn Glu Ala Arg Leu Glu Ala Asn Val Arg
70 75 80 85

gta aac gga gaa act agc ttc aag aac aaa tgg ccg agc cct ttc gcc 402
Val Asn Gly Glu Thr Ser Phe Lys Asn Lys Trp Pro Ser Pro Phe Ala
90 95 100

gta gtt tcc ggc tta ctt ctc ctc cta tcc ttc cta aag ttt gtc tac 450
Val Val Ser Gly Leu Leu Leu Leu Ser Phe Leu Lys Phe Val Tyr
105 110 115

tcg cct tta cgt tgg ctc gcc gtg gca gca gtt gcc gcc ggt atc tat 498
Ser Pro Leu Arg Trp Leu Ala Val Ala Val Ala Ala Gly Ile Tyr
120 125 130

ccg att ctt gcc aaa gcc ttt gct tcc att aaa agg cct agg atc gac 546
Pro Ile Leu Ala Lys Ala Phe Ala Ser Ile Lys Arg Pro Arg Ile Asp
135 140 145

atc aac ata ttg gtc ata ata acc gtg att gca aca ctt gca atg caa 594
Ile Asn Ile Leu Val Ile Ile Thr Val Ile Ala Thr Leu Ala Met Gln
150 155 160 165

gat ttc atg gag gca gca gca gtt gtg ttc cta ttc acc ata tcc gac		642	
Asp Phe Met Glu Ala Ala Ala Val Val Phe Leu Phe Thr Ile Ser Asp			
170	175	180	
tgg ctc gaa aca aga gct agc tac aag gcg acc tcg gta atg cag tct		690	
Trp Leu Glu Thr Arg Ala Ser Tyr Lys Ala Thr Ser Val Met Gln Ser			
185	190	195	
ctg atg agc tta gct cca caa aag gct ata ata gca gag act ggt gaa		738	
Leu Met Ser Leu Ala Pro Gln Lys Ala Ile Ile Ala Glu Thr Gly Glu			
200	205	210	
gaa gtt gaa gta gat gag gtt aag gtt gat aca gtt gta gca gtt aaa		786	
Glu Val Glu Val Asp Glu Val Lys Val Asp Thr Val Val Ala Val Lys			
215	220	225	
gct ggt gaa acc ata cca att gat gga att gtg gtg gat gga aac tgt		834	
Ala Gly Glu Thr Ile Pro Ile Asp Gly Ile Val Val Asp Gly Asn Cys			
230	235	240	245
gag gta gac gag aaa acc tta acg ggc gaa gca ttt cct gtg cct aaa		882	
Glu Val Asp Glu Lys Thr Leu Thr Gly Glu Ala Phe Pro Val Pro Lys			
250	255	260	
cag aga gat tct acg gtt tgg gct ggc acc atc aat cta aat ggt tac		930	
Gln Arg Asp Ser Thr Val Trp Ala Gly Thr Ile Asn Leu Asn Gly Tyr			
265	270	275	
ata tgt gtg aaa aca act tct tta gcg ggt gat tgc gtg gtt gcg aaa		978	
Ile Cys Val Lys Thr Thr Ser Leu Ala Gly Asp Cys Val Val Ala Lys			
280	285	290	
atg gct aag cta gta gaa gaa gct cag agc agt aaa acc aaa tct cag		1026	
Met Ala Lys Leu Val Glu Ala Gln Ser Ser Lys Thr Lys Ser Gln			
295	300	305	
aga cta ata gac aaa tgt tct cag tac tat act cca gca atc atc tta		1074	
Arg Leu Ile Asp Lys Cys Ser Gln Tyr Tyr Thr Pro Ala Ile Ile Leu			
310	315	320	325
gta tca gct tgc gtt gcc att gtc ccg gtt ata atg aag gtc cac aac		1122	
Val Ser Ala Cys Val Ala Ile Val Pro Val Ile Met Lys Val His Asn			
330	335	340	
ctt aaa cat tgg ttc cac cta gca tta gtt gtg tta gtc agt ggt tgt		1170	
Leu Lys His Trp Phe His Leu Ala Leu Val Val Leu Val Ser Gly Cys			
345	350	355	
ccc tgt ggt ctt atc ctc tct aca cca gtt gct act ttc tgt gca ctt		1218	
Pro Cys Gly Leu Ile Leu Ser Thr Pro Val Ala Thr Phe Cys Ala Leu			
360	365	370	
act aaa gcg gca act tca ggg ctt ctg atc aaa agt gct gat tat ctt		1266	
Thr Lys Ala Ala Thr Ser Gly Leu Leu Ile Lys Ser Ala Asp Tyr Leu			
375	380	385	
gac aca ctc tca aag atc aag att gtt gct ttc gat aaa act ggg act		1314	

Asp Thr Leu Ser Lys Ile Lys Ile Val Ala Phe Asp Lys Thr Gly Thr			
390	395	400	405
att aca aga gga gag ttc att gtc ata gat ttc aag tca ctc tct aga			1362
Ile Thr Arg Gly Glu Phe Ile Val Ile Asp Phe Lys Ser Leu Ser Arg			
410	415	420	
gat ata aac cta cgc agc ttg ctt tac tgg gta tca agt gtt gaa agc			1410
Asp Ile Asn Leu Arg Ser Leu Leu Tyr Trp Val Ser Ser Val Glu Ser			
425	430	435	
aaa tca agt cat cca atg gca gca aca atc gtg gat tat gca aaa tct			1458
Lys Ser Ser His Pro Met Ala Ala Thr Ile Val Asp Tyr Ala Lys Ser			
440	445	450	
gtt tct gtt gag cct agg cct gaa gag gtt gag gat tac cag aac ttt			1506
Val Ser Val Glu Pro Arg Pro Glu Glu Val Glu Asp Tyr Gln Asn Phe			
455	460	465	
cca ggt gaa gga atc tac ggg aag att gat ggt aac gat atc ttc att			1554
Pro Gly Glu Gly Ile Tyr Gly Lys Ile Asp Gly Asn Asp Ile Phe Ile			
470	475	480	485
ggg aac aaa aag ata gct tct cga gct ggt tgt tca aca gtt cca gag			1602
Gly Asn Lys Lys Ile Ala Ser Arg Ala Gly Cys Ser Thr Val Pro Glu			
490	495	500	
att gaa gtt gat acc aaa ggc ggg aag act gtt gga tac gtc tat gta			1650
Ile Glu Val Asp Thr Lys Gly Gly Lys Thr Val Gly Tyr Val Tyr Val			
505	510	515	
ggt gaa aga cta gct gga ttt ttc aat ctt tct gat gct tgt aga tct			1698
Gly Glu Arg Leu Ala Gly Phe Phe Asn Leu Ser Asp Ala Cys Arg Ser			
520	525	530	
ggt gtt tct caa gca atg gca gaa ctg aaa tct cta gga atc aaa acc			1746
Gly Val Ser Gln Ala Met Ala Glu Leu Lys Ser Leu Gly Ile Lys Thr			
535	540	545	
gca atg cta acg gga gat aat caa gcc gcg gca atg cat gct caa gaa			1794
Ala Met Leu Thr Gly Asp Asn Gln Ala Ala Ala Met His Ala Gln Glu			
550	555	560	565
cag cta ggg aat gtt tta gat gtt gta cat gga gat ctt ctt cca gaa			1842
Gln Leu Gly Asn Val Leu Asp Val Val His Gly Asp Leu Leu Pro Glu			
570	575	580	
gat aag tcc aga atc ata caa gag ttt aag aaa gag gga cca acc gca			1890
Asp Lys Ser Arg Ile Ile Gln Glu Phe Lys Lys Glu Gly Pro Thr Ala			
585	590	595	
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Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Thr Ala Asp			
600	605	610	
att ggt atc tcc atg gga att tct ggc tct gct ctt gca aca caa act			1986
Ile Gly Ile Ser Met Gly Ile Ser Gly Ser Ala Leu Ala Thr Gln Thr			

615	620	625	
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630	635	640	645
gtg aag cta gcg aga aga gca cga cgc aaa gtt gtt gaa aac gtg tgt Val Lys Leu Ala Arg Arg Ala Arg Arg Lys Val Val Glu Asn Val Cys			2082
650	655	660	
cta tcg atc att tta aaa gca gga ata ctc gct ttg gca ttt gct ggt Leu Ser Ile Ile Leu Lys Ala Gly Ile Leu Ala Leu Ala Phe Ala Gly			2130
665	670	675	
cat cct ttg att tgg gct gcg gtt ctt gtt gat gta ggg act tgt ctg His Pro Leu Ile Trp Ala Ala Val Leu Val Asp Val Gly Thr Cys Leu			2178
680	685	690	
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695	700	705	
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710	715	720	725
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730	735	740	
tta aca aag agc ggg aat ggt caa tgc aaa tca agc tgt tgt gga gat Leu Thr Lys Ser Gly Asn Gly Gln Cys Lys Ser Ser Cys Cys Gly Asp			2370
745	750	755	
aag aaa aat caa gag aac gtt gtg atg atg aaa cca agt agt aaa acc Lys Lys Asn Gln Glu Asn Val Val Met Met Lys Pro Ser Ser Lys Thr			2418
760	765	770	
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775	780	785	
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790	795	800	805
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